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1

SEQUENCE LISTING

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<141> 2001-11-29

<150> 09/604,957

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<170> PatentIn Ver. 2.1

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Asp Lys Asn Ser Thr Ser Thr Pro Val Ser Val Leu Pro Ser Asn Asn  
 100 105 110

Thr Glu Lys Gln Ala Lys Asn Tyr Asn Glu Gln Asp Lys Gly Asn Tyr  
 115 120 125

Gly Asn Ile Asp Thr Ala Tyr Phe Ser Asn Asn Gln Leu His Val Ser  
 130 135 140

Gly Trp Asn Ala Thr Asn Ala Ser Gln Gly Thr Asn Ser Arg Gln Ile  
 145 150 155 160

Ile Val Arg Asp Ile Thr Thr Asn Asn Glu Leu Gly Arg Thr Asp Val  
 165 170 175

Thr Asn Asn Val Ala Arg Pro Asp Val Lys Asn Val His Asn Val Tyr  
 180 185 190

Asn Ala Asp Asn Ser Gly Phe Asp Val Asn Val Asn Ile Asp Phe Ser  
 195 200 205

Lys Met Lys Asp Tyr Arg Asp Ser Ile Glu Ile Val Ser Arg Tyr Ser  
 210 215 220

Gly Asn Gly Lys Ser Val Asp Trp Trp Ser Gln Pro Ile Thr Phe Asp  
 225 230 235 240

Lys Asn Asn Tyr Ala Tyr Leu Asp Thr Phe Glu Val Lys Asn Gly Glu  
 245 250 255

Leu His Ala Thr Gly Trp Asn Ala Thr Asn Ser Ala Ile Asn Tyr Asn  
 260 265 270

His His Phe Val Ile Leu Phe Asp Gln Thr Asn Gly Lys Glu Val Ala  
 275 280 285

Arg Gln Glu Val Arg Glu Gly Gln Ser Arg Pro Asp Val Ala Lys Val  
 290 295 300  
 Tyr Pro Gln Val Val Gly Ala Ala Asn Ser Gly Phe Asn Val Thr Phe  
 305 310 315 320  
 Asn Ile Ser Asp Leu Asp Tyr Thr His Gln Tyr Gln Val Leu Ser Arg  
 325 330 335  
 Tyr Ser Asn Ser Asp Asn Gly Glu Gly Asp Asn Val Thr Tyr Trp Phe  
 340 345 350  
 Asn Pro Gln Ser Ile Ala Pro Ala Asn Gln Ser Asn Gln Gly Tyr Leu  
 355 360 365  
 Asp Ser Phe Asp Ile Ser Lys Asn Gly Glu Val Thr Val Thr Gly Trp  
 370 375 380  
 Asn Ala Thr Asp Leu Ser Glu Leu Gln Asn Asn His Tyr Val Ile Leu  
 385 390 395 400  
 Phe Asp Gln Thr Ala Gly Lys Gln Val Ala Ser Ala Lys Ala Asp Leu  
 405 410 415  
 Ile Ser Arg Pro Asp Val Ala Lys Ala Tyr Pro Thr Val Lys Thr Ala  
 420 425 430  
 Thr Asn Ser Gly Phe Lys Val Thr Phe Lys Val Asn Asn Leu Gln Pro  
 435 440 445  
 Gly His Gln Tyr Ser Val Val Ser Arg Phe Ser Ala Asp Glu Asn Gly  
 450 455 460  
 Asn Gly Asn Asp Lys Arg His Thr Asp Tyr Trp Phe Ser Pro Val Ile  
 465 470 475 480  
 Leu Asn Gln Thr Ala Ser Asn Ile Asp Thr Ile Thr Met Thr Ser Asn  
 485 490 495  
 Gly Leu His Ile Ala Gly Trp Met Ala Ser Asp Asn Ser Ile Asn Glu  
 500 505 510  
 Thr Thr Pro Tyr Ala Ile Ile Leu Asn Asn Gly Lys Glu Val Thr Arg  
 515 520 525  
 Gln Lys Met Ser Leu Thr Ala Arg Pro Asp Val Ala Ala Val Tyr Pro  
 530 535 540  
 Ser Leu Tyr Asn Ser Ala Val Ser Gly Phe Asp Thr Thr Ile Lys Leu  
 545 550 555 560  
 Thr Asn Asp Gln Tyr Gln Ala Leu Asn Gly Gln Leu Gln Val Leu Leu  
 565 570 575  
 Arg Phe Ser Lys Ala Ala Asp Gly Asn Pro Ser Gly Asp Asn Thr Val  
 580 585 590

Thr Asp Gln Phe Ser Lys Asn Tyr Ala Thr Thr Gly Gly Asn Phe Asp  
 595 600 605  
 Tyr Val Lys Val Asn Gly Asn Gln Val Glu Phe Ser Gly Trp His Ala  
 610 615 620  
 Thr Asn Gln Ser Asn Asp Lys Asp Ser Gln Trp Ile Ile Val Leu Val  
 625 630 635 640  
 Asn Gly Lys Glu Val Lys Arg Gln Leu Val Asn Asp Thr Lys Glu Gly  
 645 650 655  
 Ala Ala Gly Phe Asn Arg Asn Asp Val Tyr Lys Val Asn Pro Ala Ile  
 660 665 670  
 Glu Asn Ser Ser Met Ser Gly Phe Gln Gly Ile Ile Thr Leu Pro Val  
 675 680 685  
 Thr Val Lys Asn Glu Asn Val Gln Leu Val His Arg Phe Ser Asn Asp  
 690 695 700  
 Val Lys Thr Gly Glu Gly Asn Tyr Val Asp Phe Trp Ser Glu Leu Met  
 705 710 715 720  
 Pro Val Lys Asp Ser Phe Gln Lys Gly Asn Gly Pro Leu Lys Gln Phe  
 725 730 735  
 Gly Leu Gln Thr Ile Asn Gly Gln Gln Tyr Tyr Ile Asp Pro Thr Thr  
 740 745 750  
 Gly Gln Pro Arg Lys Asn Phe Leu Leu Gln Ser Gly Asn Asn Trp Ile  
 755 760 765  
 Tyr Phe Asp Ser Asp Thr Gly Val Gly Thr Asn Ala Leu Glu Leu Gln  
 770 775 780  
 Phe Ala Lys Gly Thr Val Ser Ser Asn Glu Gln Tyr Arg Asn Gly Asn  
 785 790 795 800  
 Ala Ala Tyr Ser Tyr Asp Asp Lys Ser Ile Glu Asn Val Asn Gly Tyr  
 805 810 815  
 Leu Thr Ala Asp Thr Trp Tyr Arg Pro Lys Gln Ile Leu Lys Asp Gly  
 820 825 830  
 Thr Thr Trp Thr Asp Ser Lys Glu Thr Asp Met Arg Pro Ile Leu Met  
 835 840 845  
 Val Trp Trp Pro Asn Thr Leu Thr Gln Ala Tyr Tyr Leu Asn Tyr Met  
 850 855 860  
 Lys Gln His Gly Asn Leu Leu Pro Ser Ala Leu Pro Phe Phe Asn Ala  
 865 870 875 880  
 Asp Ala Asp Pro Ala Glu Leu Asn His Tyr Ser Glu Ile Val Gln Gln  
 885 890 895

Asn Ile Glu Lys Arg Ile Ser Glu Thr Gly Asn Thr Asp Trp Leu Arg  
 900 905 910  
 Thr Leu Met His Asp Phe Val Thr Asn Asn Pro Met Trp Asn Lys Asp  
 915 920 925  
 Ser Glu Asn Val Asn Phe Ser Gly Ile Gln Phe Gln Gly Gly Phe Leu  
 930 935 940  
 Lys Tyr Glu Asn Ser Asp Leu Thr Pro Tyr Ala Asn Ser Asp Tyr Arg  
 945 950 955 960  
 Leu Leu Gly Arg Met Pro Ile Asn Ile Lys Asp Gln Thr Tyr Arg Gly  
 965 970 975  
 Gln Glu Phe Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Val Val  
 980 985 990  
 Gln Ala Glu Gln Leu Asn Trp Leu Tyr Tyr Leu Leu Asn Phe Gly Thr  
 995 1000 1005  
 Ile Thr Ala Asn Asn Asp Gln Ala Asn Phe Asp Ser Val Arg Val Asp  
 1010 1015 1020  
 Ala Pro Asp Asn Ile Asp Ala Asp Leu Met Asn Ile Ala Gln Asp Tyr  
 1025 1030 1035 1040  
 Phe Asn Ala Ala Tyr Gly Met Asp Ser Asp Ala Val Ser Asn Lys His  
 1045 1050 1055  
 Ile Asn Ile Leu Glu Asp Trp Asn His Ala Asp Pro Glu Tyr Phe Asn  
 1060 1065 1070  
 Lys Ile Gly Asn Pro Gln Leu Thr Met Asp Asp Thr Ile Lys Asn Ser  
 1075 1080 1085  
 Leu Asn His Gly Leu Ser Asp Ala Thr Asn Arg Trp Gly Leu Asp Ala  
 1090 1095 1100  
 Ile Val His Gln Ser Leu Ala Asp Arg Glu Asn Asn Ser Thr Glu Asn  
 1105 1110 1115 1120  
 Val Val Ile Pro Asn Tyr Ser Phe Val Arg Ala His Asp Asn Asn Ser  
 1125 1130 1135  
 Gln Asp Gln Ile Gln Asn Ala Ile Arg Asp Val Thr Gly Lys Asp Tyr  
 1140 1145 1150  
 His Thr Phe Thr Phe Glu Asp Glu Gln Lys Gly Ile Asp Ala Tyr Ile  
 1155 1160 1165  
 Gln Asp Gln Asn Ser Thr Val Lys Lys Tyr Asn Leu Tyr Asn Ile Pro  
 1170 1175 1180  
 Ala Ser Tyr Ala Ile Leu Leu Thr Asn Lys Asp Thr Ile Pro Arg Val  
 1185 1190 1195 1200

Tyr Tyr Gly Asp Leu Tyr Thr Asp Gly Gly Gln Tyr Met Glu His Gln  
 1205 1210 1215  
 Thr Arg Tyr Tyr Asp Thr Leu Thr Asn Leu Leu Lys Ser Arg Val Lys  
 1220 1225 1230  
 Tyr Val Ala Gly Gly Gln Ser Met Gln Thr Met Ser Val Gly Gly Asn  
 1235 1240 1245  
 Asn Asn Ile Leu Thr Ser Val Arg Tyr Gly Lys Gly Ala Met Thr Ala  
 1250 1255 1260  
 Thr Asp Thr Gly Thr Asp Glu Thr Arg Thr Gln Gly Ile Gly Val Val  
 1265 1270 1275 1280  
 Val Ser Asn Thr Pro Asn Leu Lys Leu Gly Val Asn Asp Lys Val Val  
 1285 1290 1295  
 Leu His Met Gly Ala Ala His Lys Asn Gln Gln Tyr Arg Ala Ala Val  
 1300 1305 1310  
 Leu Thr Thr Thr Asp Gly Val Ile Asn Tyr Thr Ser Asp Gln Gly Ala  
 1315 1320 1325  
 Pro Val Ala Met Thr Asp Glu Asn Gly Asp Leu Tyr Leu Ser Ser His  
 1330 1335 1340  
 Asn Leu Val Val Asn Gly Lys Glu Glu Ala Asp Thr Ala Val Gln Gly  
 1345 1350 1355 1360  
 Tyr Ala Asn Pro Asp Val Ser Gly Tyr Leu Ala Val Trp Val Pro Val  
 1365 1370 1375  
 Gly Ala Ser Asp Asn Gln Asp Ala Arg Thr Ala Pro Ser Thr Glu Lys  
 1380 1385 1390  
 Asn Ser Gly Asn Ser Ala Tyr Arg Thr Asn Ala Ala Phe Asp Ser Asn  
 1395 1400 1405  
 Val Ile Phe Glu Ala Phe Ser Asn Phe Val Tyr Thr Pro Thr Lys Glu  
 1410 1415 1420  
 Ser Glu Arg Ala Asn Val Arg Ile Ala Gln Asn Ala Asp Phe Phe Ala  
 1425 1430 1435 1440  
 Ser Leu Gly Phe Thr Ser Phe Glu Met Ala Pro Gln Tyr Asn Ser Ser  
 1445 1450 1455  
 Lys Asp Arg Thr Phe Leu Asp Ser Thr Ile Asp Asn Gly Tyr Ala Phe  
 1460 1465 1470  
 Thr Asp Arg Tyr Asp Leu Gly Met Ser Glu Pro Asn Lys Tyr Gly Thr  
 1475 1480 1485  
 Asp Glu Asp Leu Arg Asn Ala Ile Gln Ala Leu His Lys Ala Gly Leu  
 1490 1495 1500

Gln Val Met Ala Asp Trp Val Pro Asp Gln Ile Tyr Asn Leu Pro Gly  
 1505 1510 1515 1520  
 Lys Glu Val Ala Thr Val Thr Arg Val Asp Asp Arg Gly Asn Val Trp  
 1525 1530 1535  
 Lys Asp Ala Ile Ile Asn Asn Asn Leu Tyr Val Val Asn Thr Ile Gly  
 1540 1545 1550  
 Gly Gly Glu Tyr Gln Lys Lys Tyr Gly Gly Ala Phe Leu Asp Lys Leu  
 1555 1560 1565  
 Gln Lys Leu Tyr Pro Glu Ile Phe Thr Lys Lys Gln Val Ser Thr Gly  
 1570 1575 1580  
 Val Ala Ile Asp Pro Ser Gln Lys Ile Thr Glu Trp Ser Ala Lys Tyr  
 1585 1590 1595 1600  
 Phe Asn Gly Thr Asn Ile Leu His Arg Gly Ser Gly Tyr Val Leu Lys  
 1605 1610 1615  
 Ala Asp Gly Gly Gln Tyr Tyr Asn Leu Gly Thr Thr Thr Lys Gln Phe  
 1620 1625 1630  
 Leu Pro Ile Gln Leu Thr Gly Glu Lys Lys Gln Gly Asn Glu Gly Phe  
 1635 1640 1645  
 Val Lys Gly Asn Asp Gly Asn Tyr Tyr Phe Tyr Asp Leu Ala Gly Asn  
 1650 1655 1660  
 Met Val Lys Asn Thr Phe Ile Glu Asp Ser Val Gly Asn Trp Tyr Phe  
 1665 1670 1675 1680  
 Phe Asp Gln Asp Gly Lys Met Val Glu Asn Lys His Phe Val Asp Val  
 1685 1690 1695  
 Asp Ser Tyr Gly Glu Lys Gly Thr Tyr Phe Phe Leu Lys Asn Gly Val  
 1700 1705 1710  
 Ser Phe Arg Gly Gly Leu Val Gln Thr Asp Asn Gly Thr Tyr Tyr Phe  
 1715 1720 1725  
 Asp Asn Tyr Gly Lys Met Val Arg Asn Gln Thr Ile Asn Ala Gly Ala  
 1730 1735 1740  
 Met Ile Tyr Thr Leu Asp Glu Asn Gly Lys Leu Ile Lys Ala Ser Tyr  
 1745 1750 1755 1760  
 Asn Ser Asp Ala Glu Tyr Pro Thr Ser Thr Asp Val Gly Lys Met Leu  
 1765 1770 1775  
 Asp Gln Asn Lys Leu  
 1780

<210> 3  
 <211> 13

<212> PRT  
 <213> Lactobacillus reuteri

<400> 3  
 Tyr Tyr Phe Tyr Asp Leu Ala Gly Asn Met Val Lys Asn  
           1                  5                  10

<210> 4  
 <211> 13  
 <212> PRT  
 <213> Lactobacillus reuteri

<400> 4  
 Trp Tyr Phe Phe Asp Gln Asp Gly Lys Met Val Glu Asn  
           1                  5                  10

<210> 5  
 <211> 13  
 <212> PRT  
 <213> Lactobacillus reuteri

<400> 5  
 Thr Tyr Tyr Phe Asp Asn Tyr Gly Lys Met Val Arg Asn  
           1                  5                  10

<210> 6  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<220>  
 <221> modified\_base  
 <222> (9)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (15)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (18)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 6  
 gayaakwsna aksynrtngt nsargc



<210> 7  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<220>  
 <221> modified\_base  
 <222> (2)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (5)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (8)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (17)  
 <223> a, t, c or g

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 7  
 gnkcncanat ratrcnctr na

22

<210> 8  
 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 8  
 acaaccacca tggaattagg tcgcactgat gtaac

35

<210> 9  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

&lt;400&gt; 9

gccagctgga tccgtcgact agttttatttt tgatcaagca tcttacc

47

&lt;210&gt; 10

&lt;211&gt; 545

&lt;212&gt; PRT

&lt;213&gt; Streptococcus mutans

&lt;400&gt; 10

Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Val Val Gln Ala Glu  
 1 5 10 15

Gln Leu Asn Trp Leu His Tyr Leu Met Asn Tyr Gly Ser Ile Val Ala  
 20 25 30

Asn Asp Pro Glu Ala Asn Phe Asp Gly Val Arg Val Asp Ala Val Asp  
 35 40 45

Asn Val Asn Ala Asp Leu Leu Gln Ile Ala Ser Asp Tyr Leu Lys Ala  
 50 55 60

His Tyr Gly Val Asp Lys Ser Glu Lys Asn Ala Ile Asn His Leu Ser  
 65 70 75 80

Ile Leu Glu Ala Trp Ser Asp Asn Asp Pro Gln Tyr Asn Lys Asp Thr  
 85 90 95

Lys Gly Ala Gln Leu Pro Ile Asp Asn Lys Leu Arg Leu Ser Leu Leu  
 100 105 110

Tyr Ala Leu Thr Arg Pro Leu Glu Lys Asp Ala Ser Asn Lys Asn Glu  
 115 120 125

Ile Arg Ser Gly Leu Glu Pro Val Ile Thr Asn Ser Leu Asn Asn Arg  
 130 135 140

Ser Ala Glu Gly Lys Asn Ser Glu Arg Met Ala Asn Tyr Ile Phe Ile  
 145 150 155 160

Arg Ala His Asp Ser Glu Val Gln Thr Val Ile Ala Lys Ile Ile Lys  
 165 170 175

Ala Gln Ile Asn Pro Lys Thr Asp Gly Leu Thr Phe Thr Leu Asp Glu  
 180 185 190

Leu Lys Gln Ala Phe Lys Ile Tyr Asn Glu Asp Met Arg Gln Ala Lys  
 195 200 205

Lys Lys Tyr Thr Gln Ser Asn Ile Pro Thr Ala Tyr Ala Leu Met Leu  
 210 215 220

Ser Asn Lys Asp Ser Ile Thr Arg Leu Tyr Tyr Gly Asp Met Tyr Ser  
 225 230 235 240

Asp Asp Gly Gln Tyr Met Ala Thr Lys Ser Pro Tyr Tyr Asp Ala Ile  
 245 250 255

Asp Thr Leu Leu Lys Ala Arg Ile Lys Tyr Ala Ala Gly Gly Gln Asp  
 260 265 270  
 Met Lys Ile Thr Tyr Val Glu Gly Asp Lys Ser His Met Asp Trp Asp  
 275 280 285  
 Tyr Thr Gly Val Leu Thr Ser Val Arg Tyr Gly Thr Gly Ala Asn Glu  
 290 295 300  
 Ala Thr Asp Gln Gly Ser Glu Ala Thr Lys Thr Gln Gly Met Ala Val  
 305 310 315 320  
 Ile Thr Ser Asn Asn Pro Ser Leu Lys Leu Asn Gln Asn Asp Lys Val  
 325 330 335  
 Ile Val Asn Met Gly Ala Ala His Lys Asn Gln Glu Tyr Arg Pro Leu  
 340 345 350  
 Leu Leu Thr Thr Lys Asp Gly Leu Thr Ser Tyr Thr Ser Asp Ala Ala  
 355 360 365  
 Ala Lys Ser Leu Tyr Arg Lys Thr Asn Asp Lys Gly Glu Leu Val Phe  
 370 375 380  
 Asp Ala Ser Asp Ile Gln Gly Leu Tyr Leu Asn Pro Gln Val Ser Gly  
 385 390 395 400  
 Leu Ala Val Trp Val Pro Val Gly Ala Ser Asp Asn Gln Asp Val Arg  
 405 410 415  
 Val Ala Ala Ser Asn Lys Ala Asn Ala Thr Gly Gln Val Tyr Glu Ser  
 420 425 430  
 Ser Ser Ala Leu Asp Ser Gln Leu Ile Tyr Glu Gly Phe Ser Asn Phe  
 435 440 445  
 Gln Asp Phe Val Thr Lys Asp Ser Asp Tyr Thr Asn Lys Lys Ile Ala  
 450 455 460  
 Gln Asn Val Gln Leu Phe Lys Ser Trp Gly Val Thr Ser Phe Glu Met  
 465 470 475 480  
 Ala Pro Gln Tyr Val Ser Ser Glu Asp Gly Ser Phe Leu Asp Ser Ile  
 485 490 495  
 Ile Gln Asn Gly Tyr Ala Phe Glu Asp Arg Tyr Asp Leu Ala Met Ser  
 500 505 510  
 Lys Asn Asn Lys Tyr Gly Ser Gln Gln Asp Met Ile Asn Ala Val Lys  
 515 520 525  
 Ala Leu His Lys Ser Gly Ile Gln Val Ile Ala Asp Trp Val Pro Asp  
 530 535 540  
 Gln  
 545

<210> 11  
 <211> 522  
 <212> PRT  
 <213> Leuconostoc mesenteroides

<400> 11

Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Val Val Val Glu Ala Glu  
 1 5 10 15  
 Gln Leu Asn Trp Leu Tyr Tyr Leu Met Asn Phe Gly Thr Ile Thr Ala  
 20 25 30  
 Asn Asp Ala Asp Ala Asn Phe Asp Gly Ile Arg Val Asp Ala Val Asp  
 35 40 45  
 Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Ala Asp Tyr Phe Lys Leu  
 50 55 60  
 Ala Tyr Gly Val Asp Gln Asn Asp Ala Thr Ala Asn Gln His Leu Ser  
 65 70 75 80  
 Ile Leu Glu Asp Trp Ser His Asn Asp Pro Leu Tyr Val Thr Asp Gln  
 85 90 95  
 Gly Ser Asn Gln Leu Thr Met Asp Asp Tyr Val His Thr Gln Leu Ile  
 100 105 110  
 Trp Ser Leu Thr Lys Ser Ser Asp Ile Arg Gly Thr Met Gln Arg Phe  
 115 120 125  
 Val Asp Tyr Tyr Met Val Asp Arg Ser Asn Asp Ser Thr Glu Asn Glu  
 130 135 140  
 Ala Ile Pro Asn Tyr Ser Phe Val Arg Ala His Asp Ser Glu Val Gln  
 145 150 155 160  
 Thr Val Ile Ala Gln Ile Val Ser Asp Leu Tyr Pro Asp Val Glu Asn  
 165 170 175  
 Ser Leu Ala Pro Thr Thr Glu Gln Leu Ala Ala Ala Phe Lys Val Tyr  
 180 185 190  
 Asn Glu Asp Glu Lys Leu Ala Asp Lys Lys Tyr Thr Gln Tyr Asn Met  
 195 200 205  
 Ala Ser Ala Tyr Ala Met Leu Leu Thr Asn Lys Asp Thr Val Pro Arg  
 210 215 220  
 Tyr Tyr Gly Asp Leu Tyr Thr Asp Asp Gly Gln Tyr Met Ala Thr Lys  
 225 230 235 240  
 Ser Pro Tyr Tyr Asp Ala Ile Asn Thr Leu Leu Lys Ala Arg Val Gln  
 245 250 255  
 Tyr Val Ala Gly Gly Gln Ser Met Ser Val Asp Ser Asn Asp Val Leu  
 260 265 270

Thr Ser Val Arg Tyr Gly Lys Asp Ala Met Thr Ala Ser Asp Thr Gly  
275 280 285

Thr Ser Glu Thr Arg Thr Glu Gly Ile Gly Val Ile Val Ser Asn Asn  
290 295 300

Ala Glu Leu Gln Leu Glu Asp Gly His Thr Val Thr Leu His Met Gly  
305 310 315 320

Ala Ala His Lys Asn Gln Ala Tyr Arg Ala Leu Leu Ser Thr Thr Ala  
325 330 335

Asp Gly Leu Ala Tyr Tyr Asp Thr Asp Glu Asn Ala Pro Val Ala Tyr  
340 345 350

Thr Asp Ala Asn Gly Asp Leu Ile Phe Thr Asn Glu Ser Ile Tyr Gly  
355 360 365

Val Gln Asn Pro Gln Val Ser Gly Tyr Leu Ala Val Trp Val Pro Val  
370 375 380

Gly Ala Gln Gln Asp Gln Asp Ala Arg Thr Ala Ser Asp Thr Thr Thr  
385 390 395 400

Asn Thr Ser Asp Lys Val Phe His Ser Asn Ala Ala Leu Asp Ser Gln  
405 410 415

Val Ile Tyr Glu Gly Phe Ser Asn Phe Gln Ala Phe Ala Thr Asp Ser  
420 425 430

Ser Glu Tyr Thr Asn Val Val Ile Ala Gln Asn Ala Asp Gln Phe Lys  
435 440 445

Gln Trp Gly Val Thr Ser Phe Gln Leu Ala Pro Gln Tyr Arg Ser Ser  
450 455 460

Thr Asp Thr Ser Phe Leu Asp Ser Ile Ile Gln Asn Gly Tyr Ala Phe  
465 470 475 480

Thr Asp Arg Tyr Asp Leu Gly Tyr Gly Thr Pro Thr Lys Tyr Gly Thr  
485 490 495

Ala Asp Gln Leu Arg Asp Ala Ile Lys Ala Leu His Ala Ser Gly Ile  
500 505 510

Gln Ala Ile Ala Asp Trp Val Pro Asp Gln  
515 520

<210> 12

<211> 584

<212> PRT

<213> Leuconostoc mesenteroides

<400> 12

Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Ile Val Gln Ala Glu  
1 5 10 15

Gln Leu Asn Trp Leu His Tyr Leu Met Asn Phe Gly Ser Ile Thr Gly  
 20 25 30  
 Asn Asn Asp Asn Ala Asn Phe Asp Gly Ile Arg Val Asp Ala Val Asp  
 35 40 45  
 Asn Val Asp Ala Asp Leu Leu Lys Ile Ala Gly Asp Tyr Phe Lys Ala  
 50 55 60  
 Leu Tyr Gly Thr Asp Lys Ser Asp Ala Asn Ala Asn Lys His Leu Ser  
 65 70 75 80  
 Ile Leu Glu Asp Trp Asn Gly Lys Asp Pro Gln Tyr Val Asn Gln Gln  
 85 90 95  
 Gly Asn Ala Gln Leu Thr Met Asp Tyr Thr Val Thr Ser Gln Phe Gly  
 100 105 110  
 Asn Ser Leu Thr His Gly Ala Asn Asn Arg Ser Asn Met Trp Tyr Phe  
 115 120 125  
 Leu Asp Thr Gly Tyr Tyr Leu Asn Gly Asp Leu Asn Lys Lys Ile Val  
 130 135 140  
 Asp Lys Asn Arg Pro Asn Ser Gly Thr Leu Val Asn Arg Ile Ala Asn  
 145 150 155 160  
 Ser Gly Asp Thr Lys Val Ile Pro Asn Tyr Ser Phe Val Arg Ala His  
 165 170 175  
 Asp Tyr Asp Ala Gln Asp Pro Ile Arg Lys Ala Met Ile Asp His Gly  
 180 185 190  
 Ile Ile Lys Asn Met Gln Asp Thr Phe Thr Phe Asp Gln Leu Ala Gln  
 195 200 205  
 Gly Met Glu Phe Tyr Tyr Lys Asp Gln Glu Asn Pro Ser Gly Phe Lys  
 210 215 220  
 Lys Tyr Asn Asp Tyr Asn Leu Pro Ser Ala Tyr Ala Met Leu Leu Thr  
 225 230 235 240  
 Asn Lys Asp Thr Val Pro Arg Val Tyr Tyr Gly Asp Met Tyr Leu Glu  
 245 250 255  
 Gly Gly Gln Tyr Met Glu Lys Gly Thr Ile Tyr Asn Pro Val Ile Ser  
 260 265 270  
 Ala Leu Leu Lys Ala Arg Ile Lys Tyr Val Ser Gly Gly Gln Thr Met  
 275 280 285  
 Ala Thr Asp Ser Ser Gly Lys Asp Leu Lys Asp Gly Glu Thr Asp Leu  
 290 295 300  
 Leu Thr Ser Val Arg Phe Gly Lys Gly Ile Met Thr Ser Asp Gln Thr  
 305 310 315 320

Thr Thr Gln Asp Asn Ser Gln Asp Tyr Lys Asn Gln Gly Ile Gly Val  
 325 330 335  
 Ile Val Gly Asn Asn Pro Asp Leu Lys Leu Asn Asn Asp Lys Thr Ile  
 340 345 350  
 Thr Leu His Met Gly Lys Ala His Lys Asn Gln Leu Tyr Arg Ala Leu  
 355 360 365  
 Val Leu Ser Asn Asp Ser Gly Ile Asp Val Tyr Asp Ser Asp Asp Lys  
 370 375 380  
 Ala Pro Thr Leu Arg Thr Asn Asp Asn Gly Asp Leu Ile Phe His Lys  
 385 390 395 400  
 Thr Asn Thr Phe Val Lys Gln Asp Gly Thr Ile Ile Asn Tyr Glu Met  
 405 410 415  
 Lys Gly Ser Leu Asn Ala Leu Ile Ser Gly Tyr Leu Gly Val Trp Val  
 420 425 430  
 Pro Val Gly Ala Ser Asp Ser Gln Asp Ala Arg Thr Val Ala Thr Glu  
 435 440 445  
 Ser Ser Ser Ser Asn Asp Gly Ser Val Phe His Ser Asn Ala Ala Leu  
 450 455 460  
 Asp Ser Asn Val Ile Tyr Glu Gly Phe Ser Asn Phe Gln Ala Met Pro  
 465 470 475 480  
 Thr Ser Pro Glu Gln Ser Thr Asn Val Val Ile Ala Thr Lys Ala Asn  
 485 490 495  
 Leu Phe Lys Glu Leu Gly Ile Thr Ser Phe Glu Leu Ala Pro Gln Tyr  
 500 505 510  
 Arg Ser Ser Gly Asp Thr Asn Tyr Gly Gly Met Ser Phe Leu Asp Ser  
 515 520 525  
 Phe Leu Asn Asn Gly Tyr Ala Phe Thr Asp Arg Tyr Asp Leu Gly Phe  
 530 535 540  
 Asn Lys Ala Asp Gly Asn Pro Asn Pro Thr Lys Tyr Gly Thr Asp Gln  
 545 550 555 560  
 Asp Leu Arg Asn Ala Ile Glu Ala Leu His Lys Asn Gly Met Gln Ala  
 565 570 575  
 Ile Ala Asp Trp Val Pro Asp Gln  
 580

&lt;210&gt; 13

&lt;211&gt; 535

&lt;212&gt; PRT

&lt;213&gt; Lactobacillus reuteri

&lt;400&gt; 13

Leu Leu Ala Asn Asp Ile Asp Asn Ser Asn Pro Val Val Gln Ala Glu  
 1 5 10 15

Gln Leu Asn Trp Leu Tyr Tyr Leu Leu Asn Phe Gly Thr Ile Thr Ala  
 20 25 30

Asn Asn Asp Gln Ala Asn Phe Asp Ser Val Arg Val Asp Ala Pro Asp  
 35 40 45

Asn Ile Asp Ala Asp Leu Met Asn Ile Ala Gln Asp Tyr Phe Asn Ala  
 50 55 60

Ala Tyr Gly Met Asp Ser Asp Ala Val Ser Asn Lys His Ile Asn Ile  
 65 70 75 80

Leu Glu Asp Trp Asn His Ala Asp Pro Glu Tyr Phe Asn Lys Ile Gly  
 85 90 95

Asn Pro Gln Leu Thr Met Asp Asp Thr Ile Lys Asn Ser Leu Asn His  
 100 105 110

Gly Leu Ser Asp Ala Thr Asn Arg Trp Gly Leu Asp Ala Ile Val His  
 115 120 125

Gln Ser Leu Ala Asp Arg Glu Asn Asn Ser Thr Glu Asn Val Val Ile  
 130 135 140

Pro Asn Tyr Ser Phe Val Arg Ala His Asp Asn Asn Ser Gln Asp Gln  
 145 150 155 160

Ile Gln Asn Ala Ile Arg Asp Val Thr Gly Lys Asp Tyr His Thr Phe  
 165 170 175

Thr Phe Glu Asp Glu Gln Lys Gly Ile Asp Ala Tyr Ile Gln Asp Gln  
 180 185 190

Asn Ser Thr Val Lys Lys Tyr Asn Leu Tyr Asn Ile Pro Ala Ser Tyr  
 195 200 205

Ala Ile Leu Leu Thr Asn Lys Asp Thr Ile Pro Arg Val Tyr Tyr Gly  
 210 215 220

Asp Leu Tyr Thr Asp Gly Gly Gln Tyr Met Glu His Gln Thr Arg Tyr  
 225 230 235 240

Tyr Asp Thr Leu Thr Asn Leu Leu Lys Ser Arg Val Lys Tyr Val Ala  
 245 250 255

Gly Gly Gln Ser Met Gln Thr Met Ser Val Gly Gly Asn Asn Asn Ile  
 260 265 270

Leu Thr Ser Val Arg Tyr Gly Lys Gly Ala Met Thr Ala Thr Asp Thr  
 275 280 285

Gly Thr Asp Glu Thr Arg Thr Gln Gly Ile Gly Val Val Val Ser Asn  
 290 295 300



Thr Pro Asn Leu Lys Leu Gly Val Asn Asp Lys Val Val Leu His Met  
 305 310 315 320  
 Gly Ala Ala His Lys Asn Gln Gln Tyr Arg Ala Ala Val Leu Thr Thr  
 325 330 335  
 Thr Asp Gly Val Ile Asn Tyr Thr Ser Asp Gln Gly Ala Pro Val Ala  
 340 345 350  
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 Tyr Asp Leu Gly Met Ser Glu Pro Asn Lys Tyr Gly Thr Asp Glu Asp  
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